



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Björck, Lars
Sjöbring, Ulf
- (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Seed IP Law Group
 - (B) STREET: 701 Fifth Avenue Suite 6300
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/325,278
 - (B) FILING DATE: 26-OCT-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Potter, Jane E. R.
 - (B) REGISTRATION NUMBER: 33,332
 - (C) REFERENCE/DOCKET NUMBER: 100084.402
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Glu | Asn | Lys | Glu | Glu | Thr | Pro | Glu | Thr | Pro | Glu | Thr | Asp | Ser | 1 | 5 | 10 | 15 |
| Glu | Glu | Glu | Val | Thr | Ile | Lys | Ala | Asn | Leu | Ile | Phe | Ala | Asn | Gly | Ser | 20 | 25 | 30 | |
| Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | Thr | Phe | Glu | Lys | Ala | Thr | Ser | Glu | 35 | 40 | 45 | |
| Ala | Tyr | Ala | Tyr | Ala | Asp | Thr | Leu | Lys | Lys | Asp | Asn | Gly | Glu | Tyr | Thr | 50 | 55 | 60 | |
| Val | Asp | Val | Ala | Asp | Lys | Gly | Tyr | Thr | Leu | Asn | Ile | Lys | Phe | Ala | Gly | 65 | 70 | 75 | 80 |
| Lys | Glu | Lys | Thr | Pro | Glu | Glu | Pro | Lys | Glu | Glu | Val | Thr | Ile | Lys | Ala | 85 | 90 | 95 | |
| Asn | Leu | Ile | Tyr | Ala | Asp | Gly | Lys | Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | 100 | 105 | 110 | |
| Thr | Phe | Glu | Glu | Ala | Thr | Ala | Glu | Ala | Tyr | Arg | Tyr | Ala | Asp | Ala | Leu | 115 | 120 | 125 | |
| Lys | Lys | Asp | Asn | Gly | Glu | Tyr | Thr | Val | Asp | Val | Ala | Asp | Lys | Gly | Tyr | 130 | 135 | 140 | |
| Thr | Leu | Asn | Ile | Lys | Phe | Ala | Gly | Lys | Glu | Lys | Thr | Pro | Glu | Glu | Pro | 145 | 150 | 155 | 160 |
| Lys | Glu | Glu | Val | Thr | Ile | Lys | Ala | Asn | Leu | Ile | Tyr | Ala | Asp | Gly | Lys | 165 | 170 | 175 | |
| Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | Thr | Phe | Glu | Glu | Ala | Thr | Ala | Glu | 180 | 185 | 190 | |
| Ala | Tyr | Arg | Tyr | Ala | Asp | Leu | Leu | Ala | Lys | Glu | Asn | Gly | Lys | Tyr | Thr | 195 | 200 | 205 | |
| Val | Asp | Val | Ala | Asp | Lys | Gly | Tyr | Thr | Leu | Asn | Ile | Lys | Phe | Ala | Gly | 210 | 215 | 220 | |
| Lys | Glu | Lys | Thr | Pro | Glu | Glu | Pro | Lys | Glu | Glu | Val | Thr | Ile | Lys | Ala | 225 | 230 | 235 | 240 |
| Asn | Leu | Ile | Tyr | Ala | Asp | Gly | Lys | Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | 245 | 250 | 255 | |
| Thr | Phe | Ala | Glu | Ala | Thr | Ala | Glu | Ala | Tyr | Arg | Tyr | Ala | Asp | Leu | Leu | 260 | 265 | 270 | |
| Ala | Lys | Glu | Asn | Gly | Lys | Tyr | Thr | Ala | Asp | Leu | Glu | Asp | Gly | Gly | Tyr | 275 | 280 | 285 | |

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
 290 295 300

Glu
 305

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|--|-----|
| GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA | 60 |
| ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAAGTGCAGA ATTCAAAGGA | 120 |
| ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT | 180 |
| GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA | 240 |
| AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT | 300 |
| GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA | 360 |
| GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA | 420 |
| GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA | 480 |
| AAAGAAGAAG TTACTATTAA AGCAAACCTA ATCTATGCAG ATGGAAAAAC ACAACAGCA | 540 |
| GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGAAGTTATTA | 600 |
| GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT | 660 |
| AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA | 720 |
| AACTTAATCT ATGCAGATGG AAAAAGTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA | 780 |
| GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA | 840 |
| GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC | 900 |
| GAAAAACCAG AAGAATAATA A | 921 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Glu | Asn | Lys | Glu | Glu | Thr | Pro | Glu | Thr | Pro | Glu | Thr | Asp | Ser | 1 | 5 | 10 | 15 |
| Glu | Glu | Glu | Val | Thr | Ile | Lys | Ala | Asn | Leu | Ile | Phe | Ala | Asn | Gly | Ser | 20 | 25 | 30 | |
| Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | Thr | Phe | Glu | Lys | Ala | Thr | Ser | Glu | 35 | 40 | 45 | |
| Ala | Tyr | Ala | Tyr | Ala | Asp | Thr | Leu | Lys | Lys | Asp | Asn | Gly | Glu | Tyr | Thr | 50 | 55 | 60 | |
| Val | Asp | Val | Ala | Asp | Lys | Gly | Tyr | Thr | Leu | Asn | Ile | Lys | Phe | Ala | Gly | 65 | 70 | 75 | 80 |
| Lys | Glu | Lys | Thr | Pro | Glu | Glu | Pro | Lys | Glu | Glu | Val | Thr | Ile | Lys | Ala | 85 | 90 | 95 | |
| Asn | Leu | Ile | Tyr | Ala | Asp | Gly | Lys | Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | 100 | 105 | 110 | |
| Thr | Phe | Glu | Glu | Ala | Thr | Ala | Glu | Ala | Tyr | Arg | Tyr | Ala | Asp | Ala | Leu | 115 | 120 | 125 | |
| Lys | Lys | Asp | Asn | Gly | Glu | Tyr | Thr | Val | Asp | Val | Ala | Asp | Lys | Gly | Tyr | 130 | 135 | 140 | |
| Thr | Leu | Asn | Ile | Lys | Phe | Ala | Gly | Lys | Glu | Lys | Thr | Pro | Glu | Glu | Pro | 145 | 150 | 155 | 160 |
| Lys | Glu | Glu | Val | Thr | Ile | Lys | Ala | Asn | Leu | Ile | Tyr | Ala | Asp | Gly | Lys | 165 | 170 | 175 | |
| Thr | Gln | Thr | Ala | Glu | Phe | Lys | Gly | Thr | Phe | Glu | Glu | Ala | Thr | Ala | Glu | 180 | 185 | 190 | |
| Ala | Tyr | Arg | Tyr | Ala | Asp | Leu | Leu | Ala | Lys | Glu | Asn | Gly | Lys | Tyr | Thr | 195 | 200 | 205 | |

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 210 215 220
 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 225 230 235 240
 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 245 250 255
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 260 265 270
 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 275 280 285
 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
 290 295 300
 Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
 305 310 315 320
 Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
 325 330 335
 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
 340 345 350
 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
 355 360 365
 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
 370 375 380
 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
 385 390 395 400
 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
 405 410 415
 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
 420 425 430
 Glu Met

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli* L392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|--|------|
| GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA | 60 |
| ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AACTGCAGA ATTCAAAGGA | 120 |
| ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT | 180 |
| GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA | 240 |
| AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT | 300 |
| GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA | 360 |
| GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA | 420 |
| GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA | 480 |
| AAAGAAGAAG TTACTATTAA AGCAAACCTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA | 540 |
| GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGAAGTATTA | 600 |
| GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT | 660 |
| AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAG AAGAAGTTAC TATTAAAGCA | 720 |
| AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA | 780 |
| GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA | 840 |
| GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC | 900 |
| GAAAAACCAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA AACATTGAAA | 960 |
| GGCGAAACAA CTAAGTGAAGC TGTTGATGCT GCTACTGCAG AAAAAGTCTT CAAACAATAC | 1020 |
| GCTAACGACA ACGGTGTTGA CGGTGAATGG ACTTACGACG ATGCGACTAA GACCTTTACA | 1080 |
| GTTACTGAAA AACCAGAAGT GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACTTAC | 1140 |
| AAACTTGTTA TTAATGGTAA AACATTGAAA GGCGAAACAA CTAATAAGC AGTAGACGCA | 1200 |
| GAAACTGCAG AAAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA TGGTGTGTTG | 1260 |
| ACTTATGATG ATGCGACTAA GACCTTTACG GTAAGTAAA TGTAATAA | 1308 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC | 48 |
| Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn | |
| 1 5 10 15 | |
| AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA | 96 |
| Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu | |
| 20 25 30 | |
| AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG | 144 |
| Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys | |
| 35 40 45 | |
| AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT | 192 |
| Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg | |
| 50 55 60 | |
| AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA | 240 |
| Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu | |
| 65 70 75 80 | |
| GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA | 288 |
| Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu | |
| 85 90 95 | |
| GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG | 336 |
| Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg | |
| 100 105 110 | |
| GAC TAC CAT AGA GCT ACC GCT TTA GAA AAA GAG TTA GAA GAG AAA AAG | 384 |
| Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Glu Lys Lys | |
| 115 120 125 | |
| AAA GCT CTT GAA TTA GCG ATA GAC CAA GCG AGT CAG GAC TAT AAT AGA | 432 |
| Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg | |
| 130 135 140 | |
| GCT AAC GTC TTA GAA AAA GAG TTA GAA ACG ATT ACT AGA GAA CAA GAG | 480 |
| Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu | |
| 145 150 155 160 | |
| ATT AAT CGT AAT CTT TTA GGC AAT GCA AAA CTT GAA CTT GAT CAA CTT | 528 |
| Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu | |

| | | | | 165 | | | | 170 | | | | 175 | | | | | | | |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|------|--|--|--|
| TCA Ser | TCT Ser | GAA Glu | AAA Lys 180 | GAG Glu | CAG Gln | CTA Leu | ACG Thr | ATC Ile 185 | GAA Glu | AAA Lys | GCA Ala | AAA Lys | CTT Leu 190 | GAG Glu | GAA Glu | 576 | | | |
| GAA Glu | AAA Lys | CAA Gln 195 | ATC Ile | TCA Ser | GAC Asp | GCA Ala | AGT Ser 200 | CGT Arg | CAA Gln | AGC Ser | CTT Leu | CGT Arg 205 | CGT Arg | GAC Asp | TTG Leu | 624 | | | |
| GAC Asp | GCA Ala 210 | TCA Ser | CGT Arg | GAA Glu | GCT Ala | AAG Lys 215 | AAA Lys | CAG Gln | GTT Val | GAA Glu | AAA Lys 220 | GAT Asp | TTA Leu | GCA Ala | AAC Asn | 672 | | | |
| TTG Leu 225 | ACT Thr | GCT Ala | GAA Glu | CTT Leu | GAT Asp 230 | AAG Lys | GTT Val | AAA Lys | GAA Glu | GAC Asp 235 | AAA Lys | CAA Gln | ATC Ile | TCA Ser | GAC Asp 240 | 720 | | | |
| GCA Ala | AGC Ser | CGT Arg | CAA Gln | CGG Arg 245 | CTT Leu | CGC Arg | CGT Arg | GAC Asp | TTG Leu 250 | GAC Asp | GCA Ala | TCA Ser | CGT Arg | GAA Glu 255 | GCT Ala | 768 | | | |
| AAG Lys | AAA Lys | CAG Gln 260 | GTT Val | GAA Glu | AAA Lys | GAT Asp | TTA Leu | GCA Ala 265 | AAC Asn | TTG Leu | ACT Thr | GCT Ala 270 | GAA Glu | CTT Leu | GAT Asp | 816 | | | |
| AAG Lys | GTT Val 275 | AAA Lys | GAA Glu | GAA Glu | AAA Lys | CAA Gln | ATC Ile 280 | TCA Ser | GAC Asp | GCA Ala | AGC Ser | CGT Arg 285 | CAA Gln | CGG Arg | CTT Leu | 864 | | | |
| CGC Arg | CGT Arg 290 | GAC Asp | TTG Leu | GAC Asp | GCA Ala | TCA Ser 295 | CGT Arg | GAA Glu | GCT Ala | AAG Lys | AAA Lys 300 | CAA Gln | GTT Val | GAA Glu | AAA Lys | 912 | | | |
| GCT Ala 305 | TTA Leu | GAA Glu | GAA Glu | GCA Ala | AAC Asn 310 | AGC Ser | AAA Lys | TTA Leu | GCT Ala | GCT Ala 315 | CTT Leu | GAA Glu | AAA Lys | CTT Leu | AAC Asn 320 | 960 | | | |
| AAA Lys | GAG Glu | CTT Leu | GAA Glu | GAA Glu | AGC Ser 325 | AAG Lys | AAA Lys | TTA Leu | ACA Thr 330 | GAA Glu | AAA Lys | GAA Glu | AAA Lys 335 | GCT Ala | GAA Glu | 1008 | | | |
| CTA Leu | CAA Gln | GCA Ala | AAA Lys 340 | CTT Leu | GAA Glu | GCA Ala | GAA Glu | GCA Ala | AAA Lys 345 | GCA Ala | CTC Leu | AAA Lys | GAA Glu 350 | CAA Gln | TTA Leu | 1056 | | | |
| GCG Ala | AAA Lys | CAA Gln 355 | GCT Ala | GAA Glu | GAA Glu | CTC Leu | GCA Ala 360 | AAA Lys | CTA Leu | AGA Arg | GCT Ala | GGA Gly 365 | AAA Lys | GCA Ala | TCA Ser | 1104 | | | |
| GAC Asp | TCA Ser 370 | CAA Gln | ACC Thr | CCT Pro | GAT Asp | ACA Thr 375 | AAA Lys | CCA Pro | GGA Gly | AAC Asn | AAA Lys 380 | GCT Val | CTT Leu | CCA Pro | GGT Gly | 1152 | | | |
| AAA Lys 385 | GGT Gly | CAA Gln | GCA Ala | CCA Pro | CAA Gln 390 | GCA Ala | GGT Gly | ACA Thr | AAA Lys | CCT Pro 395 | AAC Asn | CAA Gln | AAC Asn | AAA Lys | GCA Ala 400 | 1200 | | | |

| | |
|---|------|
| CCA ATG AAG GAA ACT AAG AGA CAG TTA CCA TCA ACA GGT GAA ACA GCT | 1248 |
| Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala | |
| 405 410 415 | |
| AAC CCA TTC TTC ACA GCG GCA CGC GTT ACT GTT ATG GCA ACA GCT GGA | 1296 |
| Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly | |
| 420 425 430 | |
| GTA GCA GCA GTT GTA AAA CGC AAA GAA GAA AAC TAA | 1332 |
| Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn | |
| 435 440 | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|---|--|
| Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn | |
| 1 5 10 15 | |
| Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu | |
| 20 25 30 | |
| Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys | |
| 35 40 45 | |
| Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg | |
| 50 55 60 | |
| Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu | |
| 65 70 75 80 | |
| Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu | |
| 85 90 95 | |
| Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg | |
| 100 105 110 | |
| Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Glu Lys Lys | |
| 115 120 125 | |
| Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg | |
| 130 135 140 | |
| Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu | |
| 145 150 155 160 | |
| Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu | |
| 165 170 175 | |

Ser Ser Glu Lys Glu Gln Leu Thr Ile Glu Lys Ala Lys Leu Glu Glu
 180 185 190
 Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Ser Leu Arg Arg Asp Leu
 195 200 205
 Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys Asp Leu Ala Asn
 210 215 220
 Leu Thr Ala Glu Leu Asp Lys Val Lys Glu Asp Lys Gln Ile Ser Asp
 225 230 235 240
 Ala Ser Arg Gln Arg Leu Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala
 245 250 255
 Lys Lys Gln Val Glu Lys Asp Leu Ala Asn Leu Thr Ala Glu Leu Asp
 260 265 270
 Lys Val Lys Glu Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Arg Leu
 275 280 285
 Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys
 290 295 300
 Ala Leu Glu Glu Ala Asn Ser Lys Leu Ala Ala Leu Glu Lys Leu Asn
 305 310 315 320
 Lys Glu Leu Glu Glu Ser Lys Lys Leu Thr Glu Lys Glu Lys Ala Glu
 325 330 335
 Leu Gln Ala Lys Leu Glu Ala Glu Ala Lys Ala Leu Lys Glu Gln Leu
 340 345 350
 Ala Lys Gln Ala Glu Glu Leu Ala Lys Leu Arg Ala Gly Lys Ala Ser
 355 360 365
 Asp Ser Gln Thr Pro Asp Thr Lys Pro Gly Asn Lys Ala Val Pro Gly
 370 375 380
 Lys Gly Gln Ala Pro Gln Ala Gly Thr Lys Pro Asn Gln Asn Lys Ala
 385 390 395 400
 Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala
 405 410 415
 Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly
 420 425 430
 Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn
 435 440

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCAGGCGG CGCCGGTAGA AAATAAAGAA GAAACACCAG AAAC

44

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Glu Asn Lys Glu Glu Thr Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCAGCAGG ATTCTTATTA TTCTTCTGGT TTTTCGTCAA CTTTCTT

47

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGCAGCAGC CATGGGTTCT TCTGGTTTTT CGTCAACTTT CTTA

44

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCATGGAC ACTTACAAAT TAATCCTTAA TGGT

34

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Tyr | Lys | Leu | Ile | Leu | Asn | Gly |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGGTCGACT TATTACATTT CAGTTACCGT AAAGGTCTTA GT

42

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | |
|---|-----|
| AAGCTTAAGG AGGTTAATCG ATGAAAAAAA CTGCTATCGC TATCGCTGTT GCTCTGGCTG | 60 |
| GTTTCGCTAC TGTTGCTCAG GCGGCGCCGA GATCTAAACA GGAATTCGAG CTCGGTACCC | 120 |
| GGGGATCCTC TAGAGCTGAC CTGCAGGCAT GC | 152 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Val Glu Asn
1